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OM protein - protein search, using sw model

Run on: April 24, 2002, 10:37:58 ; Search time 71.56 Seconds  
(without alignments)  
82.491 Million cell updates/sec

Title: US-09-525-998a-2\_copy\_41\_201

Perfect score: 941

Sequence: 1 NSVCPQPKYTHPNNSDCEI.....CSNCKSLKCTKLCIPQIEN 161

Scoring table: Gapop 10.0 , Gapext 0.5

Searched: 100059 seqs, 16664827 residues

Total number of hits satisfying chosen parameters: 100059

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Swissprot\_39;\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description |
|------------|-------|-------------|--------|-------|-------------|
| 1          | 941   | 100.0       | 455    | 1     | TNRI_HUMAN  |
| 2          | 716.5 | 76.1        | 461    | 1     | TNRI_PIG    |
| 3          | 680   | 72.3        | 454    | 1     | TNRI_MOUSE  |
| 4          | 674.5 | 71.7        | 471    | 1     | TNRI_BOVIN  |
| 5          | 669   | 71.1        | 461    | 1     | TNRI_RAT    |
| 6          | 200.5 | 21.3        | 417    | 1     | WSLI_HUMAN  |
| 7          | 187.5 | 19.9        | 435    | 1     | TNRC_HUMAN  |
| 8          | 182.5 | 19.4        | 427    | 1     | NGFR_HUMAN  |
| 9          | 181   | 19.2        | 474    | 1     | TNRC_MOUSE  |
| 10         | 179.5 | 19.1        | 326    | 1     | VIC2_MXVL   |
| 11         | 178   | 18.9        | 325    | 1     | VT2_SFVKA   |
| 12         | 176.5 | 18.8        | 332    | 1     | FASA_FIG    |
| 13         | 176.5 | 18.8        | 425    | 1     | NGFR_RAT    |
| 14         | 167.5 | 17.8        | 299    | 1     | CM40_MOUSE  |
| 15         | 167.5 | 17.8        | 415    | 1     | TNRC_MOUSE  |
| 16         | 167   | 17.7        | 269    | 1     | CM40_BOVIN  |
| 17         | 166.5 | 17.7        | 323    | 1     | FASA_BOVIN  |
| 18         | 164   | 17.4        | 349    | 1     | VC22_VAPV   |
| 19         | 162.5 | 17.3        | 327    | 1     | FASA_MOUSE  |
| 20         | 161   | 17.1        | 461    | 1     | TNRC_HUMAN  |
| 21         | 147   | 15.6        | 324    | 1     | FASA_RAT    |
| 22         | 145   | 15.4        | 416    | 1     | NGFR_CHICK  |
| 23         | 142   | 15.1        | 283    | 1     | TP14_HUMAN  |
| 24         | 141   | 15.0        | 1680   | 1     | FUP2_MOUSE  |
| 25         | 139.5 | 14.8        | 259    | 1     | CM27_MOUSE  |
| 26         | 139.5 | 14.8        | 277    | 1     | CM40_HUMAN  |
| 27         | 138.5 | 14.7        | 260    | 1     | CM27_HUMAN  |
| 28         | 134   | 14.2        | 1696   | 1     | PKK5_BRACL  |
| 29         | 134   | 14.2        | 1877   | 1     | PKK5_MOUSE  |
| 30         | 133   | 14.1        | 687    | 1     | V541_GIALA  |
| 31         | 132   | 14.0        | 913    | 1     | PKK5_HUMAN  |
| 32         | 131.5 | 14.0        | 272    | 1     | CM40_MOUSE  |
| 33         | 130.5 | 13.9        | 335    | 1     | FASA_HUMAN  |

#### ALIGNMENTS

##### RESULT 1

| ID | TNRI_HUMAN   | STANDARD | PRI | 455 AA |
|----|--|----------|-----|--------|
| AC | P19438   |          |     |        |
| DT | 01-FEB-1991 (Rel. 17, Created)   |          |     |        |
| DT | 01-FEB-1991 (Rel. 17, Last sequence update)  |          |     |        |
| DT | 29-AUG-2001 (Rel. 45, Last annotation update)  |          |     |        |
| DE | TUMOR NECROSIS FACTOR RECEPTOR 1 PRECURSOR (HOMO) NECROSIS FACTOR BINDING PROTEIN 1 (TNF1) (P50) (TNF-R1) (TNF-R1) (C1120A).   |          |     |        |
| GN | TNFRSF1A OR TNFR1 OR TNFR.   |          |     |        |
| OS | Homo sapiens (Human).  |          |     |        |
| OC | Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  |          |     |        |
| OC | Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.   |          |     |        |
| OX | NCBI:taxid:9606;   |          |     |        |
| RN | [1]  |          |     |        |
| RP | SEQUENCE FROM N.A.   |          |     |        |
| RC | TISSUE-Placenta;   |          |     |        |
| EX | MEDLINE-90235285; PubMed-2158663;  |          |     |        |
| RA | Schall T.J., Lewis M., Koller K.J., Lee A., Rice G.C., Wood S.H.W., Getanada L., Granger G.A., Leont R., Raab H., Kohr W.J., Goeddel D.V., "Molecular cloning and expression of a receptor for human tumor necrosis factor." |          |     |        |
| RT | Cell 61:361-370(1990).   |          |     |        |
| RL | [2]  |          |     |        |
| RP | SEQUENCE FROM N.A.   |          |     |        |
| RC | MEDLINE-90235284; PubMed-2158662;  |          |     |        |
| RA | Loetscher H., Pan Y.-C.H., Lahn H.-W., Geatz P., Brockhaus M., Tabuchi H., Lesslauer W.  |          |     |        |
| RT | "Molecular cloning and expression of the human 55 kd tumor necrosis factor receptor."  |          |     |        |
| RL | Cell 61:351-359(1990).   |          |     |        |
| RN | [3]  |          |     |        |
| RP | SEQUENCE FROM N.A.   |          |     |        |
| RC | MEDLINE-9106021; PubMed-1698619;   |          |     |        |
| RA | Noplat Y., Knebel P., Brackhaus H., Endeibana H., Swani R., Adlerka D., Holman H., Wallach D.  |          |     |        |
| RT | "Soluble forms of tumor necrosis factor receptors (TNFRs), the cDNA for the type 1 TNF R, cloned using order and sequence data of its soluble form, encodes both the cell surface and a soluble form of the receptor."       |          |     |        |
| RL | EMBO J. 9:3259-3278(1990).   |          |     |        |
| RN | [4]  |          |     |        |
| RP | SEQUENCE FROM N.A.   |          |     |        |
| RC | MEDLINE-9106041; PubMed-1702937;   |          |     |        |
| RA | Humbert A., Meunier P., Frenkel M., Schaefer H., Etienne M., Lantz M., Green I., Hupmann R., Strickova O., Adol B.P.   |          |     |        |
| RT | "Molecular cloning and expression of human and rat tumor necrosis factor receptor chains (p60) and the soluble ligand, tumor necrosis factor-binding protein."   |          |     |        |
| RL | INA Cell Biol. 9:705-716(1990).  |          |     |        |
| RN | [5]  |          |     |        |
| RP | SEQUENCE FROM N.A.   |          |     |        |
| RC | TISSUE-Placenta;   |          |     |        |
| EX | MEDLINE-9101509; PubMed-2170974;   |          |     |        |
| RA | Gray F.W., Barrett K., Chaffry J., Butler M., Feldman M.   |          |     |        |
| RT | "Cloning of human tumor necrosis factor (TNF) receptor cDNA and  |          |     |        |

|    |       |      |      |   |            |                    |
|----|-------|------|------|---|------------|--------------------|
| 34 | 129   | 13.7 | 595  | 1 | CM40_HUMAN | 128508 homo sapien |
| 35 | 124   | 13.2 | 2672 | 1 | LMLE_ZALIE | 21313 caenorhabdi  |
| 36 | 122.5 | 12.9 | 271  | 1 | CM40_RAT   | 115255 rattus norv |
| 37 | 119   | 12.6 | 276  | 1 | SLI3_MOUSE | 70444 mus muscula  |
| 38 | 116.5 | 12.4 | 277  | 1 | CM40_HUMAN | 143489 homo sapien |
| 39 | 116.5 | 12.4 | 892  | 1 | LDL2_XPNA  | 295088 xenopus lae |
| 40 | 116   | 12.3 | 279  | 1 | SLI3_RAT   | 095115 rattus norv |
| 41 | 115.5 | 12.3 | 1712 | 1 | NGFR_RAT   | 000918 rattus norv |
| 42 | 115   | 12.2 | 279  | 1 | SLI3_HUMAN | 214192 homo sapien |
| 43 | 115   | 12.2 | 2318 | 1 | NTC3_MOUSE | 561962 mus muscula |
| 44 | 114   | 12.1 | 1790 | 1 | LMRL_DROME | 11046 drosophila   |
| 45 | 113.5 | 12.1 | 220  | 1 | AKA_HUMA   | 148977 hydra magni |

expression of intracellular soluble TNF-binding protein.";  
Proc Natl Acad Sci U S A 87:7486-7494(1990).  
[6]  
SEQUENCE FROM N.A.  
MP01 INE:9250049; PubMed 1315717;  
Fuchs P., Strehl S., Dworak M., Himmeler A., Ambros P.F.;  
"Structure of the human TNF receptor 1 (p60) gene (TNFR1) and  
localization to chromosome 12p13.";  
Genomics 13:219-224(1992).  
[7]  
SEQUENCE OF 41-45.  
MEDLINE-90110215; PubMed-2154136;  
Fogelman H., Novick D., Wallach D.;  
"Two tumor necrosis factor-binding proteins purified from human  
urine. Evidence for immunological cross reactivity with cell surface  
tumor necrosis factor receptors.";  
J. Biol. Chem. 265:1531-1536(1990).  
[8]  
X-RAY CRYSTALLOGRAPHY (2.85 ANGSTROMS) OF 30-211 IN COMPLEX WITH TNFR1  
MEDLINE-93258809; PubMed-8487893;  
Ramer D.W., D'Arcy A., Janes W., Gentz R., Schoenfeld H.-J.,  
Proger C.W., Iotischer A., Lesslauer W.;  
"Crystal structure of the soluble human 55 kd TNF receptor-human TNF  
beta complex: implications for TNF receptor activation.";  
Cell 73:431-445(1993).  
[9]  
X-RAY CRYSTALLOGRAPHY (1.95 ANGSTROMS) OF 41-202.  
MEDLINE-97094982; PubMed-8949750;  
Nalmsmith J.H., Devine L.O., Khono H., Sprang S.K.;  
"Structures of the extracellular domain of the type I tumor necrosis  
factor receptor.";  
Structure 4:1251-1262(1996).  
-1- FUNCTION: RECEPTOR FOR TNF-ALPHA. THE ADAPTOR MOLECULE FAHD  
RECRUITS CASPASE-8 TO THE ACTIVATED RECEPTOR. THE RESULTING  
AGGREGATE CALLED THE DEATH-INDUCING SIGNALING COMPLEX (DISC)  
PERFORMS CASPASE-8 PROTEOLYTIC ACTIVATION WHICH INITIATES THE  
SUBSEQUENT CASCADE OF CASPASES (ASPARTATE-SPECIFIC CYSTEINE  
PROTEASES) MEDIATING APOPTOSIS. CONTRIBUTES TO THE INDUCTION OF  
NONCYTOTOXIC TNF EFFECTS INCLUDING ANTI-VIRAL STATE AND ACTIVATION  
OF THE ACID SPHINGOMYELINASE.  
-1- SUBUNIT: TNF BINDING TO THE EXTRACELLULAR DOMAIN OF TNFR1 LEADS TO  
HOMOTRIMERIZATION. ONCE AGGREGATED THE RECEPTORS DEATH DOMAINS  
PROVIDE A NOVEL MOLECULAR INTERFACE THAT INTERACTS SPECIFICALLY  
WITH THE DEATH DOMAIN OF TRADD VARIOUS TRADD-INTERACTING  
PROTEINS SUCH AS TRAFs, RIP AND POSSIBLY FAHD, ASP RECRUITED TO  
TNFR1 COMPLEX BY THEIR ASSOCIATION WITH TRADD. THIS COMPLEX  
ACTIVATES AT LEAST TWO DISTINCT SIGNALING CASCADES, APOPTOSIS AND  
NF-KAPPA B SIGNALING.  
-1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.  
-1- DOMAIN: THE DOMAIN THAT INDUCES A SMASE IS PROBABLY IDENTICAL TO  
THE DEATH DOMAIN. THE N-SMASE ACTIVATION DOMAIN (NSD) IS BOTH  
NECESSARY AND SUFFICIENT FOR ACTIVATION OF N-SMASE.  
-1- SIMILARITY: CONTAINS A LA-NGFR/TNFR-TYPE CYSTEINE-RICH REGION.  
-1- SIMILARITY: CONTAINS I DEATH DOMAIN.  
-1- DATABASE: NAME-PROTEIN NOTE-CD guide CD120a entry;  
WWW="http://www.ri-fs.slm.nih.gov/ftrwcd/cd120a.htm"  
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EMBL: X55313; CAA39021.1; -  
EMBL: M33294; AAA04210.1; -  
EMBL: M58286; AAA46753.1; -  
EMBL: M61121; AAA46754.1; -  
EMBL: M75866; AAA61201.1; -  
EMBL: M75864; AAA61201.1; JOINED.  
EMBL: M75865; AAA61201.1; JOINED.  
EMBL: M60275; AAA46756.1; -

[illegible]

RESULT 2  
TNRI PIG

ID TNRI\_PIG STANDARD: PRT: 461 AA.  
 AC P50555;  
 DT 01-OCT-1996 (rel. 34, Created)  
 DT 01-OCT-1996 (rel. 34, Last sequence update)  
 DT 20-AUG-2001 (rel. 40, Last annotation update)  
 DE TUMOR NECROSIS FACTOR RECEPTOR 1 (TNF-R1) (TNF-R1)  
 DE (P55).  
 GN TNFRSF1A OR TNFR1.  
 OS Sus scrofa (Pig).  
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.  
 OX NCBI\_TaxID=9623;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE-Kidney;  
 RX MEDLINE=96011645; PubMed=7590278;  
 RA Suter B., Pauli U.H.;  
 RT "Cloning of the cDNA encoding the porcine p55 tumor necrosis factor receptor".  
 RL Gene 163:263-266(1995)  
 CC -!- FUNCTION: RECEPTOR FOR TNF-ALPHA. THE ADAPTOR MOLECULE FADD RECRUITS CASPASE-8 TO THE ACTIVATED RECEPTOR. THE RESULTING AGGREGATE CALLED THE DEATH-INDUCING SIGNALING COMPLEX (DISC) PERFORMS CASPASE-8 PROTEOLYTIC ACTIVATION WHICH INITIATES THE SUBSEQUENT CASCADE OF CASPASES (ASPARTATE-SPECIFIC CYSTEINE PROTEASES) MEDIATING APOPTOSIS (BY SIMILARITY).  
 CC -!- SUBUNIT: TNF BINDING TO THE EXTRACELLULAR DOMAIN OF TNFR1 LEADS TO HOMODIMERIZATION. ONCE AGGREGATED THE RECEPTORS DEATH DOMAINS PROVIDE A NOVEL MOLECULAR INTERFACE THAT INTERACTS SPECIFICALLY WITH THE DEATH DOMAIN OF TRAC. VARIOUS DEAD-INDUCING PROTEINS SUCH AS TRAFs, RIP AND POSSIBLY FADD, ARE RECRUITED TO TNFR1 COMPLEX BY THEIR ASSOCIATION WITH TRAFs. THIS COMPLEX ACTIVATES AT LEAST TWO DISTINCT SIGNALING CASCADES. APOPTOSIS AND NF-KAPPA B SIGNALING (BY SIMILARITY).  
 CC -!- SUBCELLULAR LOCATION: TYPE 1 MEMBRANE PROTEIN.  
 CC -!- SIMILARITY: CONTAINS A LA-NGRP/TNFR-TYPE CYSTEINE-RICH REGION.  
 CC -!- SIMILARITY: CONTAINS 1 DEATH DOMAIN.  
 CC  
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 CC  
 DR EMBL: U19994; AAC48499.1; -;  
 DR HSSD: p19438; TNFR.  
 DR InterPro: IPR000488; Death.  
 DR InterPro: IPR001368; TNFR\_c6.  
 DR Pfam: PF00531; death\_1.  
 DR Pfam: PF00202; TNFR\_c6; 3.  
 DR ProDom: P00077; TNFR\_c6; 1.  
 DR SMART: SM00005; DEATH; 1.  
 DR SMART: SM00208; TNFR\_NGFR\_1; 3.  
 DR PROSITE: PS00652; TNFR\_NGFR\_1; 3.  
 DR PROSITE: PS00650; TNFR\_NGFR\_2; 3.  
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[4]  
 RP SEQUENCE FROM N.A.  
 RC L1SSUE-Spleen;  
 RX MEDLINE-9209815; PubMed-1657766;  
 RA Kothé J.G., Brockhaus M., Gentz R., Lesslauer W.;  
 RT "Molecular cloning and expression of the mouse Tnf receptor type b";  
 RL Immunogenetics 34:338-340(1991).  
 RN [5]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE-94245292; PubMed-8188324;  
 RA Hebo R.F., Linthicum D.S.;  
 RT "Nucleotide sequence of the TNF type I receptor from a mouse  
 endometrial cell line";  
 RL Immunogenetics 39:450-451(1994).  
 RN [6]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE-93156721; PubMed-8381516;  
 RA Kothé J., Bluetmann H., Gentz R., Lesslauer W., Steinmetz M.;  
 RT "Genomic organization and promoter function of the murine tumor  
 necrosis factor receptor beta gene";  
 RL Mol. Immunol. 30:165-175(1993).  
 CC -!- FUNCTION: RECEPTOR FOR TNF-ALPHA. THE ADAPTOR MOLECULE FADD  
 RECRUITS CASPASE-8 TO THE ACTIVATED RECEPTOR. THE RESULTING  
 AGGREGATE CALLED THE DEATH-INDUCING SIGNALING COMPLEX (DISC)  
 PERFORMS CASPASE-8 PROTEOLYTIC ACTIVATION WHICH INITIATES THE  
 SUBSEQUENT CASCADE OF CASPASES (ASPARTATE-SPECIFIC CYSTEINE  
 PROTEASES) MEDIATING APOPTOSIS (BY SIMILARITY).  
 CC -!- SUBUNIT: TNF BINDING TO THE EXTRACELLULAR DOMAIN OF TNFR1 LEADS TO  
 HOMOTRIMERIZATION. ONCE AGGREGATED THE RECEPTORS DEATH DOMAINS  
 PROVIDE A NOVEL MOLECULAR INTERFACIAL THAT INTERACTS SPECIFICALLY  
 WITH THE DEATH DOMAIN OF TRADD. VARIOUS TRADD-INTERACTING  
 PROTEINS SUCH AS TRAFs, FIP AND POSSIBLY FADD, ARE RECRUITED TO  
 TNFR1 COMPLEX BY THEIR ASSOCIATION WITH TRADD. THIS COMPLEX  
 ACTIVATES AT LEAST TWO DISTINCT SIGNALING CASCADES, APOPTOSIS AND  
 NF-KAPPA B SIGNALING (BY SIMILARITY).  
 CC -!- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.  
 CC -!- SIMILARITY: CONTAINS A LA-NGFR/TNFR-TYPE CYSTEINE-REPEAT REGION.  
 CC -!- SIMILARITY: CONTAINS 1 DEATH DOMAIN.  
 CC This SWISS-PROT entry is copyrighted. It is produced through a collaboration  
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 the European Bioinformatics Institute. There are no restrictions on its  
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 entities requires a license agreement (See <http://www.isb-sib.ch/announce/>  
 or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
 DR EMBL: M60468; AAA34751.1; -;  
 DR EMBL: M59377; AAA40464.1; -;  
 DR EMBL: X59238; CAA41922.1; -;  
 DR EMBL: X57796; CAA40436.1; -;  
 DR EMBL: L26349; AAA53361.1; -;  
 DR EMBL: M76656; AAA40465.1; -;  
 DR EMBL: M88067; AAA40465.1; JOINED.  
 DR EMBL: M76655; AAA40465.1; JOINED.  
 DR PIR: A38634; GOMST1.  
 DR PIR: S16677; S16677.  
 DR PIR: S14021; S14021.  
 DR HSS: P19438; IEX1.  
 DR MGD: M611314884; Tr1rsfla.  
 DR InterPro: IPR000488; Death.  
 DR InterPro: IPR001368; TNFR\_c6.  
 DR Pfam: PF00541; death\_1.  
 DR Pfam: PF00020; TNFR\_c6; 4.  
 DR ProDom: PD000771; TNFR\_c6; 1.  
 DR SMART: SM00905; DEATH; 1.  
 DR SMART: SM00208; TNFR; 1.  
 DR PROSITE: PS00652; TNFR\_NGFR\_1; 3.  
 DR PROSITE: PS50050; TNFR\_NGFR\_2; 3.  
 DR PROSITE: PS50017; DEATH\_DOMAIN; 1.  
 KW Receptor; Transmembrane; glycoprotein; Repeat; Signal; Apoptosis.  
 FT SIGNAL 1 21 POTENTIAL.  
 FT CHAIN 22 454 TUMOR NECROSIS FACTOR RECEPTOR 1.

FT DOMAIN 22 212 EXTRA-CELLULAR (POTENTIAL).  
 FT TRANSMEM 213 235 POTENTIAL.  
 FT DOMAIN 236 454 CYTOPLASMIC (POTENTIAL).  
 FT REPEAT 43 196 4 X TNFR-CYS.  
 FT REPEAT 43 82 TNFR-CYS 1.  
 FT REPEAT 83 125 TNFR-CYS 2.  
 FT REPEAT 126 166 TNFR-CYS 3.  
 FT REPEAT 167 196 TNFR-CYS 4.  
 FT DOMAIN 339 349 N-SMASE ACTIVATION DOMAIN (NSD).  
 FT DOMAIN 356 441 DEATH.  
 FT DISULFID 44 58 BY SIMILARITY.  
 FT DISULFID 59 72 BY SIMILARITY.  
 FT DISULFID 62 81 BY SIMILARITY.  
 FT DISULFID 84 99 BY SIMILARITY.  
 FT DISULFID 102 117 BY SIMILARITY.  
 FT DISULFID 105 125 BY SIMILARITY.  
 FT DISULFID 127 143 BY SIMILARITY.  
 FT DISULFID 146 158 BY SIMILARITY.  
 FT DISULFID 149 166 BY SIMILARITY.  
 FT DISULFID 168 179 BY SIMILARITY.  
 FT DISULFID 182 191 BY SIMILARITY.  
 FT DISULFID 185 195 BY SIMILARITY.  
 FT CARBOHYD 154 154 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 151 151 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 202 202 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CONFLICT 394 394 R -> G (IN REF. 6).  
 SQ SEQUENCE 454 AA; 50129 MW; 0710C2B9C4C2H6D9 CRC64;  
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 Matches 112; Conservative 19; Mismatches 26; Indels 0; Gaps 0;  
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 DB 41 DSLPCKGKYVHSKNNSICCTCKHKGTYLYNDGPGQDIIHCKRCSGSPFASHNHLKCL 100  
 QY 61 GSKPKRKEQGVETSSVTRDTWGGCKKQKRYHYSNLEQCFNCSLGINSTVHLSQE 120  
 DB 101 SKTKPKRKSQVETSSVTRDTWGGCKKQKRYHYSNLEQCFNCSLGINSTVHLSQE 160  
 QY 121 KONTVCTCHAGFFLRNEKVSQSNCKKSECTKCLP 157  
 DB 161 TQNTVCTCHAGFFLRNEKVSQSNCKKSECTKCLP 197  
 RESULT 4  
 TNFR1\_BOVIN  
 ID TNFR1\_BOVIN STANDARD; PRT; 471 AA.  
 AC O19131;  
 DT 20 AUG 2001 (Rel. 40, Created)  
 DT 20-AUG-2001 (Rel. 40, Last sequence update)  
 DT 20-AUG-2001 (Rel. 40, Last annotation update)  
 DE TUMOR NECROSIS FACTOR RECEPTOR 1 PRECURSOR (P60) (TNF-R1) (TNF-R1)  
 DE (P55).  
 GN TNFRSF1A OR TNFR1.  
 OS Bos taurus (Bovine).  
 OC Eukaryota, Metazoa, Chordata, Craniata, Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;  
 OC Bovidae; Bovinae; Bos.  
 OX NCBI\_TaxID-9913;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE-Aorta;  
 RA Lee E.-K., Taylor M.J., Kehrli M.E.;  
 RT "Cloning of cDNA encoding bovine tumor necrosis factor-receptor 1  
 (TNF-R1)".  
 RL Submitted (FEB 1997) to the EMBL/GenBank/DBJ databases.  
 CC -!- FUNCTION: RECEPTOR FOR TNF-ALPHA. THE ADAPTOR MOLECULE FADD  
 RECRUITS CASPASE-8 TO THE ACTIVATED RECEPTOR. THE RESULTING  
 AGGREGATE CALLED THE DEATH-INDUCING SIGNALING COMPLEX (DISC)  
 PERFORMS CASPASE-8 PROTEOLYTIC ACTIVATION WHICH INITIATES THE  
 SUBSEQUENT CASCADE OF CASPASES (ASPARTATE-SPECIFIC CYSTEINE  
 CC







SQ SEQUENCE 435 AA: 46709 MW: 624626602295656F GRC64;  
 Query Match 19 GA: Score 187.5; DB 1; Length 435;  
 Best Local Similarity 32.7%; Pred. No. 7; 1e-09;  
 Matches 49; Conservative 17; Mismatches 7; Indels 13; Gaps 7;  
 QY 8 KYHIFQNSICCTKTHKTYLYNATGNGGQDQCRFCESGSEFTASENHRLSCSKCRK 67  
 DB 49 EYEFQHR ICYSGEPPTYYSAK--SEIKDVCATCAENSYENHMYLLTCLQCRPCDP 106  
 QY 68 EWCQVFTSPVDFVQVGFENFVPHYSNIFQCNESI---QLNCTVHLSCQE--KQ 122  
 DB 107 VMLGEIAICISKKRLTQKQGMFCAAWA---TECHQCTSLPTPTFAELKDEVGK 153  
 QY 123 NTVWT-CHNGFLFLENFVSCNKKSLK 151  
 DB 164 NNHCVPCKAGHP--QNTSSPSARQPHRC 191  
 RESULT P  
 NGFR\_HUMAN STANDARD: PRT: 427 AA.  
 AC P08138;  
 DT 01-AUG-1988 (Rel. 08, Created)  
 DT 01-AUG-1988 (Rel. 08, last sequence update)  
 DT 20-AUG-2001 (Rel. 40, last annotation update)  
 DE LOW-AFFINITY NERVE GROWTH FACTOR RECEPTOR PRECURSOR (NGF RECEPTOR)  
 DE (GPR0-LNGFR) (P75 ICD).  
 GN NGFR OR TNFRSF16.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=87051725; PubMed=1022937;  
 RA Johnson D., Lathan A., Buck C.P., Solhal A., Morgan C., Mercer E.,  
 RA Botwell M., Chao M.;  
 FT "A constitutive promoter directs expression of the human NGF receptor";  
 RL Cell 47:545-554(1986).  
 RN 121  
 RP SEQUENCE OF 1-22 FROM N.A.  
 RX MEDLINE=890496903; PubMed=2850481;  
 RA Sebail A., Patil N., Chao M.;  
 FT "A constitutive promoter directs expression of the nerve growth factor  
 receptor gene";  
 RL Mol. Cell. Biol. 8:3160-3167(1988).  
 CC 1- FUNCTION: LOW AFFINITY RECEPTOR WHICH CAN BIND TO NGF, BDNF,  
 CC NT-3, AND NT-4.  
 CC 1- SUBUNIT: NGF RECEPTOR CAN FORM A HOMODIMER THROUGH DISULFIDE  
 CC BOND FORMATION.  
 CC 1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.  
 CC 1- PM: N- AND O-GLYCOSYLATED AND IS PHOSPHORYLATED ON SERINE.  
 CC 1- SIMILARITY: CONTAINS A LA-NGFR/TNFR-TYPE CYSTEINE-RICH REGION.  
 CC 1- SIMILARITY: CONTAINS 1 DEATH DOMAIN.  
 CC  
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 CC  
 DR EMBL: M14764; AAH59544.1;  
 DR EMBL: M21621; AAA36363.1;  
 DR PIR: A25218; GOUN;  
 DR ISS: P07174; INGR.  
 DR MIM: 162010;  
 DR InterPro: IPR000488; Death.  
 DR InterPro: IPR001368; TNFR\_c6.  
 DR Pfam: PF00531; death; 1.

DR PFam: PF00020; TNFR\_c6; 4.  
 DR SMART: SM00005; DEATH; 1.  
 DR SMART: SM00208; TNFR; 3.  
 DR FCSITE: PS00652; TNFR\_NGFR\_1; 3.  
 DR PROSITE: PS50050; TNFR\_NGFR\_2; 4.  
 DR PROSITE: PS50017; DEATH\_DOMAIN; 1.  
 KW Receptor; Neurogenesis; Transmembrane; Glycoprotein; Repeat;  
 NW Phosphorylation; Signal.  
 FT SIGNAL 1 28  
 FT CHAIN 29 427 LOW-AFFINITY NERVE GROWTH FACTOR  
 FT RECEPTOR.  
 FT DOMAIN 29 250 EXTRACELLULAR (POTENTIAL).  
 FT TRANSMEM 251 272 POTENTIAL.  
 FT DOMAIN 273 427 CYTOPLASMIC (POTENTIAL).  
 FT DOMAIN 31 189 4 X TNFR-CYS.  
 FT REPEAT 31 65 TNFR-CYS 1.  
 FT REPEAT 66 107 TNFR-CYS 2.  
 FT REPEAT 108 147 TNFR-CYS 3.  
 FT REPEAT 148 189 TNFR-CYS 4.  
 FT DOMAIN 344 421 DEATH.  
 FT DISULFID 32 43 BY SIMILARITY.  
 FT DISULFID 44 57 BY SIMILARITY.  
 FT DISULFID 47 64 BY SIMILARITY.  
 FT DISULFID 67 83 BY SIMILARITY.  
 FT DISULFID 86 99 BY SIMILARITY.  
 FT DISULFID 89 107 BY SIMILARITY.  
 FT DISULFID 109 122 BY SIMILARITY.  
 FT DISULFID 125 138 BY SIMILARITY.  
 FT DISULFID 128 146 BY SIMILARITY.  
 FT DISULFID 149 164 BY SIMILARITY.  
 FT DISULFID 167 180 BY SIMILARITY.  
 FT DISULFID 170 188 BY SIMILARITY.  
 FT DOMAIN 197 248 SER/THR-RICH.  
 FT CAPROXYD 60 60 N-LINKED (GLCNAC... ) (POTENTIAL).  
 SQ SEQUENCE 427 AA: 45183 MW: 609FA143FB3D625B GRC64;  
 Query Match 19.4%; Score 182.5; DB 1; Length 427;  
 Best Local Similarity 32.1%; Pred. No. 1; 8e-08;  
 Matches 52; Conservative 25; Mismatches 62; Indels 23; Gaps 11;  
 QY 4 CPOCKYHPQNNISICCTKCHKCHGVLYNCPQDQDQCRFC--PSGSFTASENHRLHCLSC 62  
 DB 32 CPGLGLYTH--SGKCKACACNIGCGVAUFC--GANO IVCMHCLSVTFSDVVSATFCKKC 86  
 QY 83 SKPKEMQVFTSS--GVVDPPTVGVGFENFVPHYSNIFQCNESI---QLNCTVHLSCQE 120  
 DB 87 TEC---VCLQSMASAPCVPAUADVCRG---AYGVYDFTTCRCHACRVCAGSGLVVSCDP 140  
 QY 121 KONTVC-TCHAGFFIRE---NECVSCSNC-----KKSLEKIK 153  
 DB 141 KONTVCECPDGTYSDEANIVDPGLPCTVCTEDTERQLRECTR 182  
 RESULT 9  
 TNFR2\_MOUSE STANDARD: PRT: 474 AA.  
 AC P25119; P97893;  
 DT 01-MAY-1992 (Rel. 22, Created)  
 DT 01-MAY-1992 (Rel. 22, last sequence update)  
 DT 15-JUL-1999 (Rel. 38, last annotation update)  
 DE TUMOR NECROSIS FACTOR RECEPTOR 2 PRECURSOR (TNF- $\alpha$ ) (P75).  
 GN TNFRSF1B OR TNFR2 OR TNFR-2.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OX NCBI\_TaxID=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=91187885; PubMed=1849278;  
 RA Lewis M., Tartaglia L.A., Lee A., Bennett G.L., Rice G.C.,  
 RA Wong G.H., Chen E.Y., Goeddel D.V.;  
 FT "Cloning and expression of cDNAs for two distinct murine tumor



RT necrosis factor receptors demonstrate one receptor is species  
 RL specific.\*;  
 RL Proc. Natl. Acad. Sci. U.S.A. 88:2830-2834 (1991).

RN [2]  
 RX MEDLINE:91246168; PubMed 1645445;  
 RA Goodwin R.G., Anderson D., Jerzy R., Brannan C.I.,  
 RA Copeland N.G., Jenkins J.A., Smith C.A.  
 RT "Molecular cloning and expression of the type 1 and type 2 murine  
 RT receptors for tumor necrosis factor.\*;  
 RL Mol. Cell. Biol. 11:3020-3026 (1991).

RN [3]  
 RP SEQUENCE OF 1-26 FROM N.A.  
 RC STRAIN-Non-  
 RA Jacob C.G., Liu J.;  
 RL Submitted (Jan-1996) to the EMBL/Genbank/DBP databases.

RN [4]  
 RP SEQUENCE OF 1-22 FROM N.A.  
 RC LISSIE-Liver;  
 RA Kissenoughis M., Fellows R., Feldmann M., Chernajovsky Y.;  
 RL Submitted (May-1995) to the EMBL/Genbank/DBP databases  
 CC -1- FUNCTION: RECEPTOR FOR INF-ALPHA.  
 CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.  
 CC -1- SIMILARITY: CONTAINS A LA NGK/INR-TYPE CYSTEINE-RICH REGION.

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EMBL: M60469; AAA39752.1; -;  
 EMBL: M59378; AAA40463.1; -;  
 EMBL: U39488; AAA85021.1; -;  
 EMBL: X87128; CAA60618.1; -;  
 EMBL: X86634; X86634;  
 DSSP: P19438; INCF.  
 MGD: MGI:131483; T01rs1lb.  
 DR InterPro: IPR001369; TNFR\_c6;  
 DR Pfam: PF00020; TNFR\_c6; 4;  
 DR ProDom: PD000771; TNFR\_c6; 1;  
 DR SMART: SM00208; INFR\_4;  
 DP PROSITE: PS00652; TNFR\_NFRP\_1; 2;  
 DP PROSITE: PS50050; TNFR\_NFRP\_2; 3;  
 KW Receptor; Transmembrane; Glycoprotein; Repeat; Signal.

FT SIGNAL 1 22  
 FT CHAIN 23 474 TUMOR NECROSIS FACTOR RECEPTOR 2.  
 FT DOMAIN 23 258 EXTRACELLULAR (POTENTIAL).  
 FT TRANSMEM 259 268 POTENTIAL.  
 FT DOMAIN 289 474 CYTOPLASMIC (POTENTIAL).  
 FT DOMAIN 39 203 4 X INFR-CYS.  
 FT REPEAT 39 77 TNFR-CYS 1.  
 FT REPEAT 78 119 TNFR-CYS 2.  
 FT REPEAT 120 164 TNFR-CYS 3.  
 FT REPEAT 165 203 TNFR-CYS 4.  
 FT DISULFID 40 54 BY SIMILARITY.  
 FT DISULFID 55 68 BY SIMILARITY.  
 FT DISULFID 58 76 BY SIMILARITY.  
 FT DISULFID 79 94 BY SIMILARITY.  
 FT DISULFID 97 111 BY SIMILARITY.  
 FT DISULFID 101 119 BY SIMILARITY.  
 FT DISULFID 121 127 BY SIMILARITY.  
 FT DISULFID 136 145 BY SIMILARITY.  
 FT DISULFID 159 163 BY SIMILARITY.  
 FT DISULFID 166 181 BY SIMILARITY.  
 FT CARBOHYD 195 195 N-LINKED (GLCNAC... ) (POTENTIAL).  
 SEQUENCE 474 AA: 50219 MW: 452349.140553 GR044.

Query Match

19.2%, Score 181, BH 1, Length 474.

Host Local Similarity 31.7%, Pred No. 2,60,06;  
 Matches 51; Conservative 20; Mismatches 76; Indels 14; Gaps 8;  
 CY 4 \*PCGYTHPNNSTQTFQHTHYNECPPEALTEPEPTESSTTASIMHLPHEST 62  
 DB 40 QVLSRITQRAAMAMGQGVVNHFGNKSIVGACAEASMYGVVNNOFFILSS 98  
 CY 63 QKQKRMQVSSQSNQKQKQKQKQKQKQKQKQKQKQKQKQKQKQKQKQK 117  
 DB 99 SSSCTIDQVEIRACTKQNVNVCCEAGYCALRTHSSASDEAMRLSKQPGGVASS 154  
 CY 118 CQPKQNTVQCHACQFHPNPNQVSNQKQKQKQKQKQKQKQKQKQKQKQK 157  
 DB 155 RHPNPNVLEKACAPQIFSSQVLSQVWVRRHRTGILLATP 194

RESULT 10  
 V12\_MXVL  
 ID V12\_MXVL STANDARD: PRT 324 AA;  
 AC I29825;  
 DT 01-APR-1994 (Rel. 25, Created)  
 DT 01-APR-1994 (Rel. 25, Last sequence update)  
 DT 15-JUL-1999 (Rel. 38, Last annotation update)  
 DE TUMOR NECROSIS FACTOR SOLUBLE RECEPTOR PROTEIN (PRT IN 12).  
 GN 12.  
 OS Myxoma virus (strain lausanne).  
 OC Viruses; dsDNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae;  
 OC Leporipoxvirus.  
 OX NCBI\_TaxID:41530;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE:91335768; PubMed-1651597;  
 RA Upton G., Macen J.L., Schreier M., McFadden G.;  
 RT "Myxoma virus expresses a secreted protein with homology to the tumor  
 RT necrosis factor receptor gene family that contributes to viral  
 RT virulence\*;  
 RL Virology 164:370-382 (1991).

CC -1- FUNCTION: BINDS TO INF ALPHA AND HELIA. PR-BABLY PREVENTS INF TO  
 CC REACH CELLULAR TARGET AND THEREBY TEMPERING THE POTENTIAL  
 CC ANTIVIRAL EFFECTS OF THE CYTOKINE.

CC 1 SIMILARITY: CONTAINS A LA NGK/INR-TYPE CYSTEINE-RICH REGION.  
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EMBL: M55181; AAA46622.1; -;  
 EMBL: A23729; CAA01688.1; -;  
 DR EIR: A40566; GVZML.  
 DR HSSP: P19438; INCF.  
 DR InterPro: IPR001368; INFR\_c6;  
 DR Pfam: PF00020; TNFR\_c6; 2;  
 DR ProDom: PD000771; TNFR\_c6; 1;  
 DR SMART: SM00208; INFR\_4;  
 DR PROSITE: PS00652; TNFR\_NFRP\_1; 2;  
 DR PROSITE: PS50050; TNFR\_NFRP\_2; 3;  
 KW Receptor; Glycoprotein; Repeat; Signal.  
 FT SIGNAL 1 16 POTENTIAL.  
 FT CHAIN 17 426 TUMOR NECROSIS FACTOR SOLUBLE RECEPTOR.  
 FT DOMAIN 27 186 4 X INFR-CYS.  
 FT REPEAT 27 62 TNFR-CYS 1.  
 FT REPEAT 63 104 TNFR-CYS 2.  
 FT REPEAT 105 147 TNFR-CYS 3.  
 FT REPEAT 148 186 TNFR-CYS 4.  
 FT CARBOHYD 166 166 N-LINKED (GLCNAC... ) (POTENTIAL).  
 FT CARBOHYD 161 161 N-LINKED (GLCNAC... ) (POTENTIAL).  
 FT CARBOHYD 205 205 N-LINKED (GLCNAC... ) (POTENTIAL).  
 FT CARBOHYD 248 248 N-LINKED (GLCNAC... ) (POTENTIAL).  
 SEQUENCE 426 AA: 35208 MW: 46027.647294 PF GR044.

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DR PROSITE: PS00050; TNFR_NGFR_2; 1.
KW Receptor; Glycoprotein; Repeat; Signal.
FT SIGNAL 1 16
FT CHAIN 17 325
FT DOMAIN 27 186
FT REPEAT 27 62
FT REPEAT 63 104
FT REPEAT 105 147
FT REPEAT 148 186
FT CARBOHYD 105 105
FT CARBOHYD 181 181
FT CARBOHYD 205 205
FT CARBOHYD 238 238
SQ SEQUENCE 325 AA; 35132 MW; 81054039198A71E CRC64;

Query Match 18.9%; Score 178; DH 1; Length 325;
Best Local Similarity 29.6%; Pred. No. 3.4e-08;
Matches 45, Conservative 15, Mismatches 62, Indels 30, Gaps 6;

QY 13 QNNSICTCKHKGTYLYNCPGQDITCFEESGSETASENHLRHLSP-SKGRKEMQ 71
DB 34 EKGIAGCCSPGASVASHIC-GPGSDIVCSICKNHFIFASINHAACVSCRGKCTCHLS- 91
QY 72 VEISSCTVDRTVAGCKKNQYHYWSENLFQCFNCSLCLNGTVILHSCQEKQNTVCTHAG 141
DB 92 -ESQPCURTHRVGNCSSIGNVLLKGN-----GKICCAVQF-----KCPAG 142
QY 132 FFAKEMHCVSCKKK .....SLGKILK 155
DB 143 YGVSHTRAGDTLPEKPPHYTSSLSPTERC 164

RESULT 12
FASA_PIG
ID FASA_PIG STANDARD; PRT; 332 AA.
AC 077736;
DT 15-JUL-1999 (Rel. 38, Created)
DI 15-JUL-1999 (Rel. 38, Last sequence update)
DE 20-AUG-2001 (Rel. 40, Last annotation update)
DE FASO RECEPTOR PRECURSOR (APOPTOSIS-MEDIATING SURFACE ANTI-GEN FAS)
DE (APO-1 ANTIGEN) (CD95).
GN TNFRSF6 OR APT1 OR FAS.
OS Sus scrofa (Pig).
OC Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
OC Mammalia, Eutheria, Cetartiodactyla, Suina, Suidae; Sus.
OX NCBI_TaxID=9823;
RN [1]
PP SEQUENCE FROM N.A.
RA Bartling B., Hollmann T., Holly T., Schulz P., Heusch G., Darmer D.;
RT "Expression of apoptosis-associated genes in liberating and stunned
RT myocardium of pig.";
RL Submitted (JAN-1998)
CC -!- FUNCTION: RECEPTOR FOR A CYTOKINE LIGAND KNOWN AS FASL. THE
CC ADAPTOR MOLECULE RECRUITS CASPASE-8 TO THE ACTIVATED
CC SIGNALING COMPLEX (DISC) PERFORMS CASPASE-8 PROTEOLYTIC
CC ACTIVATION. ACTIVE CASPASE-8 INITIATES THE SUBSEQUENT CASCADE OF
CC CASPASES (ASPARTATE-SPECIFIC CYSTEINE PROTEASES) MEDIATING
CC APOPTOSIS. FAS-MEDIATED APOPTOSIS MAY HAVE A ROLE IN THE
CC INDUCTION OF PERIPHERAL TOLERANCE. IN THE ANTIGEN-STIMULATED
CC SOLICITUDE OF MATURE T-CELLS, OR BOTH (BY SIMILARITY).
CC -!- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
CC -!- DOMAIN: CONTAINS A DEATH DOMAIN INVOLVED IN THE BINDING OF FADD,
CC AND MAYBE TO OTHER CYTOSOLIC ADAPTOR PROTEINS.
CC -!- SIMILARITY: CONTAINS A LA-NGR/TNFR-TYPE CYSTEINE-RICH REGION.
CC -!- SIMILARITY: CONTAINS 1 DEATH DOMAIN.
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CC or send an email to license@sib-sib.ch.)
CC -----
CC EMBL: M17433; -; NOT_ANNOTATED_CDS.
CC EMBL: A23727; CAAG1687.1;
CC EMBL: B43692; B43692.
CC HSP: P19438; 1TNP.
CC IPI: P00020; TNFR_c6; TNFR_c6.
CC IPI: P00077; TNFR_c6; 2.
CC SMART: SM00208; TNFR_3.
CC PROSITE: PS00652; TNFR_NGFR_2.

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CC -----
DR EMRL: 029173; AAA68964.1; -
DR EMRL: 138423; AAH00646.1; -
DR EMRL: 030798; AA81344.1; -
DR HSSP: P25942; ICDF.
DR MG0: MG1:104875; Lbbr.
DR InterPro: IPR001368; INFR_c6.
DR Pfam: PF00020; INFR_c6; 3.
DR ProDom: PD000771; INFR_c6; 1.
DR SMART: SM00208; INFR_3.
DR PROSITE: PS00652; INFR_NFR_1; 2.
DR PROSITE: PS50050; INFR_NFR_2; 3.
KW Receptor; Transmembrane; Glycoprotein; Repeat; Signal.
FT SIGNAL 1 30 POTENTIAL.
FT CHAIN 31 415 LYMPHOTOXIN-BETA RECEPTOR.
FT DOMAIN 31 223 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 224 244 POTENTIAL.
FT DOMAIN 245 415 CYTOPLASMIC (POTENTIAL).
FT DOMAIN 42 213 4 X INFR-CYS.
FT REPEAT 42 81 INFR-CYS 1.
FT REPEAT 82 124 INFR-CYS 2.
FT REPEAT 125 170 INFR-CYS 3.
FT REPEAT 171 213 INFR-CYS 4.
FT DISULFID 43 58 BY SIMILARITY.
FT DISULFID 59 72 BY SIMILARITY.
FT DISULFID 62 80 BY SIMILARITY.
FT DISULFID 83 98 BY SIMILARITY.
FT DISULFID 101 116 BY SIMILARITY.
FT DISULFID 104 124 BY SIMILARITY.
FT DISULFID 126 132 BY SIMILARITY.
FT DISULFID 139 150 BY SIMILARITY.
FT DISULFID 142 169 BY SIMILARITY.
FT DISULFID 172 187 BY SIMILARITY.
FT CARBOHYD 40 40 N-LINKED (GLCNAC...) (POTENTIAL).
FT CARBOHYD 179 179 N-LINKED (GLCNAC...) (POTENTIAL).
SQ SEQUENCE 415 AA: 44956 MW: 298326A566AEF661 CRC64;

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Query Match 17.88; Score 167.5; DB 1; Length 415;
Best Local Similarity 27.68; Pred. No. 3,1e-07;
Matches 42; Conservative 21; Mismatches 74; Indels 15; Gaps 6;
QY 8 KYIHPNNSTCTKTKIKITLYLNICPGQDDEKDEESGSETASENULRHETSSKCRK 57
DB 49 EYEPHMD-VCCSRCPDGFVAVC-SKSDIVCKTCTHNSYNHWHLSIQICRCDI 106
QY 68 EMQWEISSTVDIVACGKFNAYHYWSENLEFCNCS-----LGLNFTVHLSVQEKQ 122
DB 107 VLAEEVAPCTSDRAKRCQPGMGSCVYLDN--ECVICEERLVLCQPGTEAVTDEIM 163
QY 123 NI---VCICHAGFFLRNEVCSCNCKSLHC 151
DB 164 DTDVNVCKPGHIE--QNTISSPRACQPHTRC 193

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Search completed: April 24, 2002, 10:49:10  
Job time: 672 sec

